Please replace the paragraph beginning at page 11, line 25 with the following amended paragraph.

Figure 2 shows the amino acid sequence of the PLS-CVB3 genome (SEQ ID NO:11) and the mIL-10-CVB3 (SEQ ID NO:12) at the site of the protease 2A cleavage (in SEQ ID NO:12, the sequence to the left of A...M is SEQ ID NO:3 and the sequence to the right of A...M is SEQ ID NO:4). In this construct, the cloning procedure has been modified to include a polylinker site (PLS) to facilitate the use of the CVB3 as a generic cloning and expression vehicle. Further modifications include non-direct repeat genetic sequences to code for the protease P2-A cleavage site in the nascent polyprotein. The amino acids donated by the PLS are underlined, while the amino acids which form the 2A cleavage recognition signal are double underlined. The sequence of the mIL-10 insertion is shown in bold.

Please replace the paragraph beginning at page 14, line 27 with the following amended paragraph.

Figure 10 shows PCR and sequence analysis of CVB3-PL2-Ad2L1. pCVB3-PL2-Ad2L1 was transfected into HeLa cells, and the resultant progeny virus (CVB3-PL2-Ad2L1, pass 1) was subsequently serially passaged in HeLa cell cultures (passes 2 to 10). Viral RNA was isolated from virus stocks at each passage, and the presence of the inserted Ad2 sequence was analyzed by PCR using primers flanking the insertion site in the CVB3 genome. Fig. 10 a: amplimers were separated by agarose gel electrophoresis. CVB3-PL2-Ad2L1, RT-PCR amplimer using chimeric viral RNA as the template; pCVB3-PL2-Ad2L1, PCR amplimer using the chimeric plasmid DNA as the template; CVB3/0, RT-PCR amplimer using the parental CVB3/0 RNA as template; neg., RT-PCR using RNA as template from uninfected HeLa cells; Marker, 100-bp DNA ladder. Fig. 10b and 10c: the sequence of the Ad2 insert-containing 446-bp amplimer (CVB3-PL2-Ad2L1) (Fig. 10b; nucleic acid sequence is SEQ ID NO:21; amino acid sequence is SEQ ID NO:22) and the sequence of the 225-bp Ad2 fragment-deleted amplimer (CVB3-PL2-Ad2L1del) (Fig. 10c; nucleotide sequence is SEQ ID NO:27; amino acid sequence is SEQ ID NO:28) were obtained after isolation of the DNA fragments from agarose gels. Sequence analysis was performed with the same primers as for the RT-PCR analysis. Numbering is based on the CVB3/0 genome (Genbank accession no. M88483).